

ence of HBsAg (overt infection), occult HBV infection (OBI, defined as presence of HBV DNA in the absence of HBsAg), might be also accounted in some non-or hypo-response cases.

**Methods & Materials:** : Sera from 120 HBsAg negative HCWs with low and moderate levels of anti-HBs, <10 IU/mL (group 1) and <100 IU/mL (group 2) respectively, were selected and were examined for OBI by sensitive real time PCR regardless of HBV serological profiles. Direct sequencing on surface genes was carried out in OBI-positive cases.

**Results:** Four (3.3%) were positive for OBI. All were negative for anti-HBc. Two of the positive cases had moderate levels of anti-HBs (10–100 IU/mL) from group 2. No significant differences were found between the two groups in terms of risk factors or serological data. No mutations were found in surface proteins of OBI cases.

**Conclusion:** OBI in these subjects might be due to other factors rather than presence of “a” determinant mutations. Health care workers with inadequate to moderate levels of anti-HBs (<100 IU/mL) following vaccination, regardless of their serological profile for HBV, should be tested for the presence of HBV DNA by sensitive molecular tests. Anti-HBc is not a reliable marker for suspicion of OBI, especially in high-risk group individuals.

<http://dx.doi.org/10.1016/j.ijid.2016.02.919>

#### Type: Poster Presentation

Final Abstract Number: 43.184

Session: Poster Session III

Date: Saturday, March 5, 2016

Time: 12:45–14:15

Room: Hall 3 (Posters & Exhibition)

#### Sero-epidemiological investigation on enterovirus 71 among population in Chengdu, China



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**Background:** Hand, foot and mouth disease (HFMD) mainly caused by enterovirus 71 (EV71) infection has become one of the major public health issues in China. Understanding of population's immunity against EV71 and the epidemic changes of enterovirus are benefit to the future therapeutic and prophylactic intervention of HFMD.

**Methods & Materials:** Multistage stratified cluster sampling method was used for the sampling. A total of 623 patients infected with EV-71 during Jan and Dec, 2014 are selected from 3 representative city circles in Chengdu. The EV71-IgG levels of all the samples were detected by enzyme-linked immunosorbent assay. Statistical data comparisons between various factors were analyzed by means of Pearson  $\chi^2$ , unpaired T-test, or Fisher's exact test. Correlation analysis is used to test the significance of the relationship between the positive rates and ages.

**Results:** It is of no statistical significance ( $P > 0.05$ ) when it comes to the differences of the antibody positive rates of EV71-IgG between male and female, circles and circles as well as urban and rural areas. The positive rates of the groups with the age ranging 0~1 (61.37%) and 1~2 (52.33%) are much higher than that of 3~4, 5~6, 7~9, 10~14,  $\geq 15$  groups, with the rates 29.89%,

22.52%, 14.54%, 11.26%, 7.33%, respectively (all  $P < 0.05$ ). The positive rate remained relatively high in preschool children aged <2 years and thereafter decreased sharply to more than 50% in individuals aged >5 years. In terms of the correlation of positive rate of EV71 of the monitoring data and age of patients, it is negatively correlated when subjects are under the age of 5 while it turns to be positive when subjects are over the age of 5.

**Conclusion:** It is clearly identified that the population with the age under 5, especially the infants aged 2 years or younger, are the focus of the prevention and control of HFMD. Our study could play an important role in the protection of susceptible population and the evaluation of the immune effect of the upcoming vaccine application.

<http://dx.doi.org/10.1016/j.ijid.2016.02.920>

#### Type: Poster Presentation

Final Abstract Number: 43.185

Session: Poster Session III

Date: Saturday, March 5, 2016

Time: 12:45–14:15

Room: Hall 3 (Posters & Exhibition)

#### Circulation of dengue virus-1 Genotype III during 2015 dengue outbreak in Arunachal Pradesh: A maiden report from Northeast India



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**Background:** Dengue is the most rapidly spreading arboviral disease in the world. Strain variations within the four dengue serotypes classify the virus into genetically distinct groups within serotypes called genotypes. Several studies have shown that disease outcome is associated with the genotype involved. Northeast Region of India comprises of 8 states and has witnessed several Dengue outbreaks in recent years. During 2015, a massive Dengue outbreak occurred in Pasighat, Arunachal Pradesh, India reporting around 2000 cases. All four serotypes have been reported from this region but studies on the genotype of the virus is lacking. This study was undertaken with an objective to elucidate the genotype of Dengue virus circulating in Arunachal Pradesh during the outbreak.

**Methods & Materials:** A total of 115 Dengue suspected samples were collected from Pasighat General Hospital, Arunachal Pradesh. Screening of Dengue NS1 antigen or Anti-Dengue IgM antibody was done depending upon the duration of sample collection and onset of symptom. IgG ELISA was done to determine whether the infection was primary or secondary. RT-PCR was performed using specific primers to amplify C-prM gene region. The obtained sequences were analyzed using BioEdit software and a phylogenetic tree was constructed in MEGA 6 software.

**Results:** Total 50 samples were Dengue positive by either NS1 or IgM ELISA of which eight (16%) cases were due to secondary infection. Dengue virus RNA was detected in 28 samples. Serotype 1 was found to be predominant during the outbreak. Phylogenetic analysis of the obtained sequences using Maximum Likelihood method and Kimura-2 parameter model revealed that the circulating Dengue virus-1 during the outbreak belonged to Genotype III.

**Conclusion:** This is the maiden report on genotyping of Dengue virus 1 from this region of India. Studies have shown that the emergence of newer dengue serotype/ genotype after a gap have always